

***Paenibacillus lutrae* sp. nov., a chitinolytic species isolated from a river otter in Castril Natural Park, Granada, Spain**

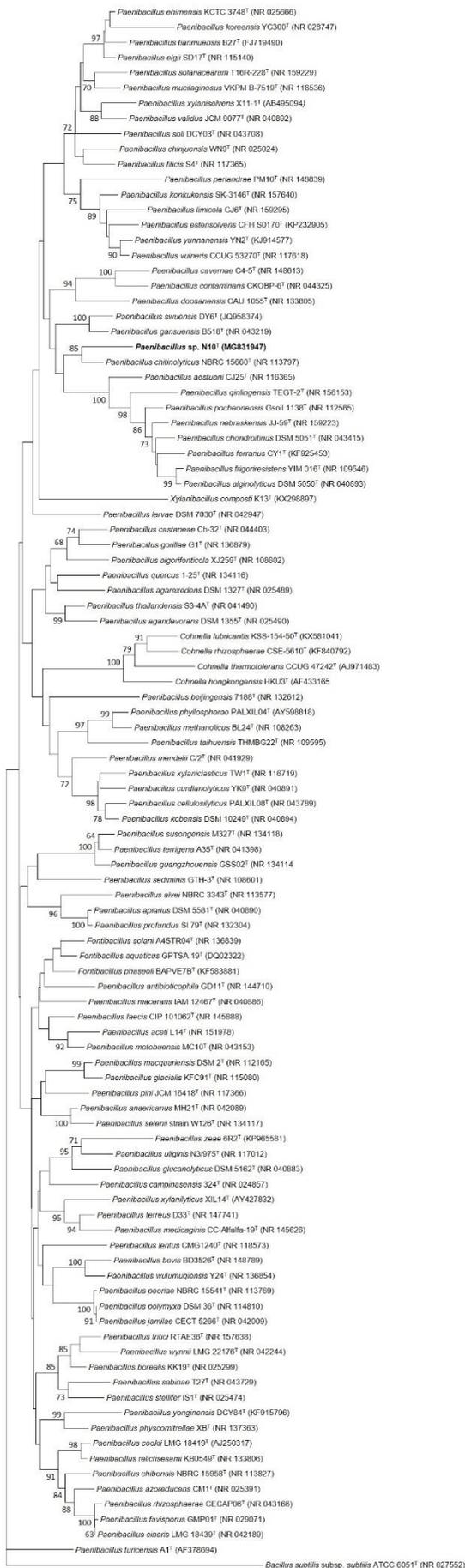
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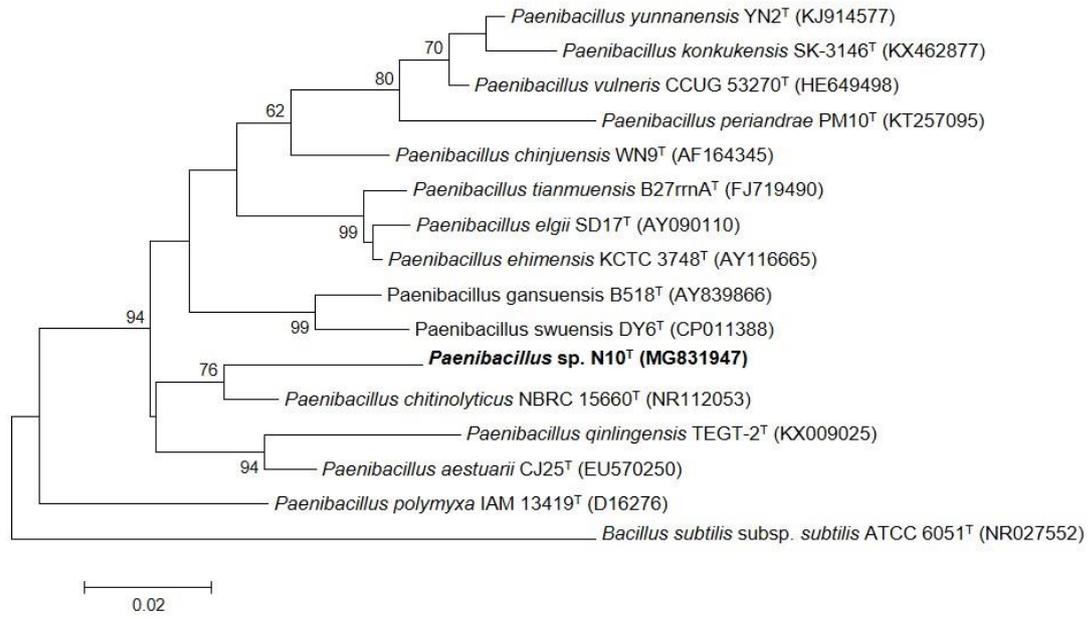
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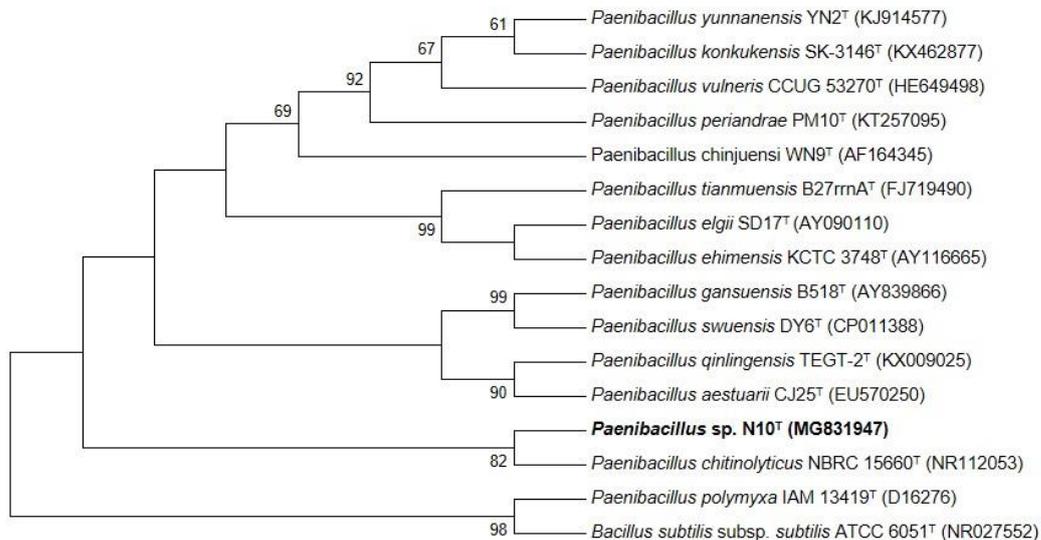
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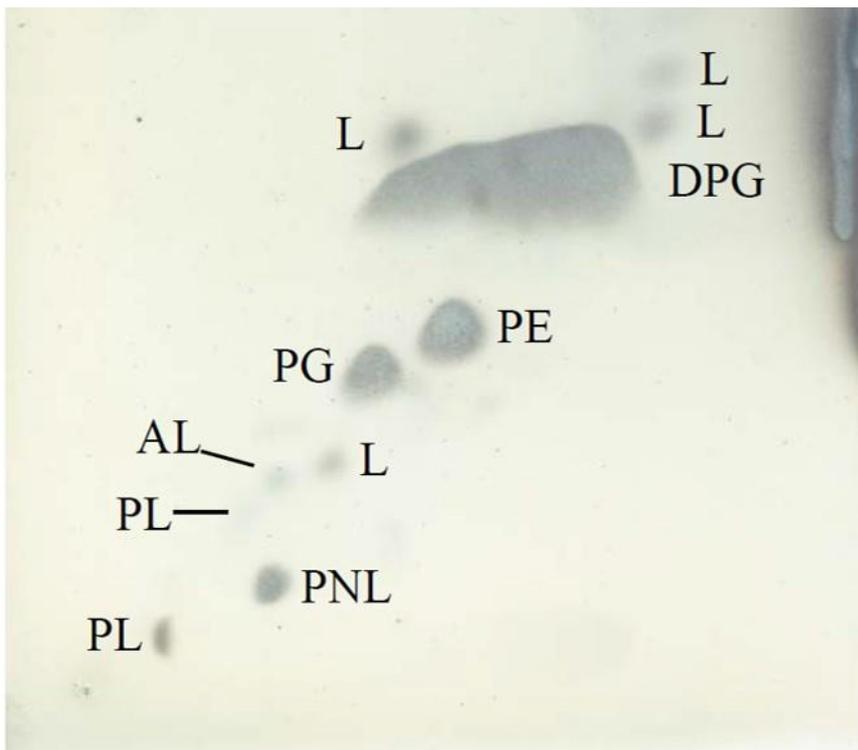
**Figure S1:** Phylogenetic position of strain N10<sup>T</sup> based on the neighbor-joining algorithm of the 16S rRNA gene sequence and its relationship with other 100 related species. The GenBank/EMBL/DDBJ accession number of each sequence is shown in parenthesis. Bootstrap values are expressed as percentages of 1,000 replications, and those greater than 60% are shown at branch points. Bar shows sequence divergence. Bar, 0.01 substitutions per nucleotide position.



**Figure S2:** Molecular phylogenetic analysis of the 16S rRNA sequence according to the maximum likelihood method. Evolutionary history was inferred using the aforementioned method based on the Jukes-Cantor model. The tree with the highest log likelihood (-5308.40) is shown. Bootstrap values are expressed as percentages of 1,000 replications, and those over 60% are shown at branch points. The *Bacillus subtilis* subsp. *subtilis* ATCC 6051<sup>T</sup> sequence was used as the outgroup.



**Figure S3:** Molecular phylogenetic analysis of the 16S rRNA sequence using the maximum parsimony method. The most parsimonious tree (length = 592) is shown. The consistency, retention and composite indices are 0.501114, 0.554672 and 0.344796 (0.277954), respectively, for all sites and parsimony-informative sites (in parentheses). Bootstrap values are expressed as percentages of 1,000 replications, and those over 60% are shown at branch points. The *Bacillus subtilis* subsp. *subtilis* ATCC 6051<sup>T</sup> sequence was used as the outgroup.



**Figure S4:** Polar lipid profile of strain N10<sup>T</sup> determined after two-dimensional TLC using molybdato-phosphoric acid. AL: aminolipid; DPG: diphosphatidylglycerol; L: lipid; PE: phosphatidylethanolamine; PG: phosphatidylglycerol; PL: phospholipid; PNL: phosphoaminolipid.

**Table S1:** ANI<sub>b</sub> and ANI<sub>m</sub> (in brackets) values among the genomes of strain N10<sup>T</sup> (1) and the most related species of *Paenibacillus* genus: *P. chitinolyticus* LMG18047<sup>T</sup> (2), *P. polymyxa* CECT155<sup>T</sup> (3), *P. elgii* SD17<sup>T</sup> (4), *P. vulneris* CCUG 53270<sup>T</sup> (5) and *P. qinlingensis* TEGT-2<sup>T</sup> (6).

Strains	1	2	3	4	5	6
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1	-	74.42 [84.64]	66.94 [86.59]	68.41 [85.80]	68.57 [85.39]	68.00 [85.46]
2	74.43 [84.64]	-	66.93 [86.68]	69.22 [85.76]	68.48 [84.88]	67.91 [87.86]
3	67.71 [86.61]	67.81 [86.66]	-	67.29 [86.34]	67.68 [85.81]	67.72 [86.66]
4	68.20 [85.77]	69.01 [85.76]	66.83 [86.33]	-	70.47 [84.62]	67.30 [85.40]
5	68.16 [85.39]	68.19 [84.88]	66.88 [85.69]	70.34 [84.59]	-	67.86 [83.75]
6	67.29 [85.44]	67.33 [87.86]	66.35 [85.94]	66.85 [85.40]	67.42 [84.69]	-

**Table S2:** Genome sequence similarity between N10<sup>T</sup> strain and genome sequences of closely related type strains with available genomes.

Strains	OrthoANI (%)	dDDH (%)
<i>P. chitinolyticus</i> LMG18047 <sup>T</sup>	75.60	21.1
<i>P. polymyxa</i> CECT155 <sup>T</sup>	68.40	31.4
<i>P. elgii</i> SD17 <sup>T</sup>	69.89	19.9
<i>P. vulneris</i> CCUG 53270 <sup>T</sup>	69.62	21.6
<i>P. qinlingensis</i> TEGT-2 <sup>T</sup>	69.19	19.3